

SEQUENCE LISTING

<110> Susanne LEONHARTSBERGER

Thomas MAIER

<120> METHOD FOR FERMENTATIVE PREPARATION OF S-ADENOSYLMETHIONINE

<130> LEONHARTSBERGER ET AL. - 1

<140> German No. 103 09 856.9

<141> 03-06-2003

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 384

<212> PRT

<213> Escherichia coli

<400> 1

Met Ala Lys His Leu Phe Thr Ser Glu Ser Val Ser Glu Gly His Pro

1

5

10

15

Asp Lys Ile Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Ile Leu

20

25

30

Leu Arg Pro Asp Ala Lys Ser Gln Val Thr Phe Gln Tyr Asp Asp Gly

165

170

175

Lys Ile Val Gly Ile Asp Ala Val Val Leu Ser Thr Gln His Ser Glu

180

185

190

Glu Ile Asp Gln Lys Ser Leu Gln Glu Ala Val Met Glu Glu Ile Ile

195

200

205

Lys Pro Ile Leu Pro Ala Glu Trp Leu Thr Ser Ala Thr Lys Phe Phe

210

215

220

Ile Asn Pro Thr Gly Arg Phe Val Ile Gly Gly Pro Met Gly Asp Cys

225

230

235

240

Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala

245

250

255

Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp

260

265

270

Arg Ser Ala Ala Tyr Ala Ala Arg Tyr Val Ala Lys Asn Ile Val Ala

275

280

285

Ala Gly Leu Ala Asp Arg Cys Glu Ile Gln Val Ser Tyr Ala Ile Gly

290

295

300

Val Ala Glu Pro Thr Ser Ile Met Val Glu Thr Phe Gly Thr Glu Lys

305

310

315

320

Val Pro Ser Glu Gln Leu Thr Leu Leu Val Arg Glu Phe Phe Asp Leu

325

330

335

Arg Pro Tyr Gly Leu Ile Gln Met Leu Asp Leu Leu His Pro Ile Tyr

340

345

350

Lys Glu Thr Ala Ala Tyr Gly His Phe Gly Arg Glu His Phe Pro Trp

355

360

365

Glu Lys Thr Asp Lys Ala Gln Leu Leu Arg Asp Ala Ala Gly Leu Lys

370

375

380

<210> 2

<211> 1155

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(1152)

<223> metK

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<306> 1453-1474

<307> 1997

<400> 2

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gcttgcgaaa cctacgtaaa aaccggcatg gtttttagttg gcggcgaaat caccaccagc 180

gcctgggtag acatcgaaga gatcacccgt aacaccgttc gcgaaattgg ctatgtgcat 240

tccgacatgg gctttgacgc taactcctgt gcggttctga gcgctatcgg caaacagtct 300

cctgacatca accagggcgt tgaccgtgcc gatccgctgg aacagggcgc gggtgaccag 360

ggctctgatgt ttggctacgc aactaatgaa accgacgtgc tgatgccagc acctatcacc 420

tatgcacacc gtctggtaca gcgtcaggct gaagtgcgta aaaacggcac tctgccgtgg 480

ctgcgcccgg acgcgaaaag ccaggtgact tttcagtatg acgacggcaa aatcgttggt 540

atcgatgctg tcgtgctttc cactcagcac tctgaagaga tcgaccagaa atcgctgcaa 600

gaagcggtaa tggaagagat catcaagcca attctgcccg ctgaatggct gacttctgcc 660

accaaattct tcatcaaccc gaccggtcgt ttcgttatcg gtggcccaat gggtgactgc 720

ggctctgactg gtcgtaaaat tatcgttgat acctacggcg gcatggcgcg tcacgggtggc 780

ggtgcaattct ctggtaaaga tccatcaaaa gtggaccgtt ccgcagccta cgcagcacgt 840

tatgtcgcga aaaacatcgt tgctgctggc ctggccgatac gttgtgaaat tcaggtttcc 900

tacgcaatcg gcgtggctga accgacctcc atcatggtag aaactttcgg tactgagaaa 960
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ctgattcaga tgctggatct gctgcacccg atctacaaag aaaccgcagc atacggtcac 1080
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gccggtctga agtaa 1155

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide metK2

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide metK4

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<210> 5

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide RLSS1

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ctagcaggag gaattcacca tgggacctgt ggatggc

37

<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide RLSS2

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gggtaccccg ctaaaacaca agcttcttgg ggacctccca

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<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide GAPDHfw

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<210> 8

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide GAPDHrevII

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<210> 9

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Multiple Cloning Site

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gaagatctag gaggcctagc atatgtgaat tcccgggctg cagctg

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<210> 10

<211> 1185

<212> DNA

<213> Rattus norvegicus

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<223> RLSS-Gen

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Met Gly Pro Val Asp Gly Leu Cys Asp His Ser Leu Ser Glu Glu Gly
1 5 10 15

gcc ttc atg ttc aca tct gaa tcg gta gga gaa ggg cat cca gat aag 96
Ala Phe Met Phe Thr Ser Glu Ser Val Gly Glu Gly His Pro Asp Lys
20 25 30

atc tgt gac cag att agt gat gca gtg ctg gat gcc cat ctc aag caa 144
Ile Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala His Leu Lys Gln
35 40 45

gac ccc aat gcc aag gtg gcc tgt gag aca gtg tgc aag aca ggg atg 192
Asp Pro Asn Ala Lys Val Ala Cys Glu Thr Val Cys Lys Thr Gly Met
50 55 60

gtg ctc ctg tgt gga gag atc acc tca atg gcc atg att gac tac cag 240
 Val Leu Leu Cys Gly Glu Ile Thr Ser Met Ala Met Ile Asp Tyr Gln
 65 70 75 80

cgg gtg gtg aga gac acc att aag cac att ggc tac gat gac tct gcc 288
 Arg Val Val Arg Asp Thr Ile Lys His Ile Gly Tyr Asp Asp Ser Ala
 85 90 95

aag ggc ttc gac ttc aag acc tgc aat gtg ctc gtg gct ctg gag caa 336
 Lys Gly Phe Asp Phe Lys Thr Cys Asn Val Leu Val Ala Leu Glu Gln
 100 105 110

cag tcc cca gac att gcc caa tgt gtc cat cta gac aga aat gag gag 384
 Gln Ser Pro Asp Ile Ala Gln Cys Val His Leu Asp Arg Asn Glu Glu
 115 120 125

gac gtt ggt gca gga gat cag ggt ctg atg ttc ggc tat gcc act gac 432
 Asp Val Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asp
 130 135 140

gag aca gag gag tgc atg ccg ctc acc att gtt ctt gct cac aaa ctc 480
 Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Val Leu Ala His Lys Leu

145	150	155	160	
aac acc cgg atg gca gat ctg agg cgc tct ggt gtc ctt ccc tgg ctg				528
Asn Thr Arg Met Ala Asp Leu Arg Arg Ser Gly Val Leu Pro Trp Leu				
	165	170	175	
aga cct gat tct aag act cag gta aca gtt cag tac gtg cag gat aat				576
Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln Tyr Val Gln Asp Asn				
	180	185	190	
ggt gct gtc atc cct gtt cgc gtc cac acc atc gtc atc tct gtg caa				624
Gly Ala Val Ile Pro Val Arg Val His Thr Ile Val Ile Ser Val Gln				
	195	200	205	
cac aac gaa gac ata aca ctg gag gcc atg cga gag gcc ctg aag gag				672
His Asn Glu Asp Ile Thr Leu Glu Ala Met Arg Glu Ala Leu Lys Glu				
	210	215	220	
cag gtg atc aaa gct gtg gtg cca gcc aag tac ctg gat gaa gac acc				720
Gln Val Ile Lys Ala Val Val Pro Ala Lys Tyr Leu Asp Glu Asp Thr				
225	230	235	240	

atc tac cac ctg cag cca agt ggg cgg ttt gtc atc gga ggt ccc cag 768
 Ile.Tyr His Leu Gln Pro Ser Gly Arg Phe Val Ile Gly Gly Pro Gln
 245 250 255

ggg gat gca ggt gtc aca ggc cgc aag att att gtg gac aca tac gga 816
 Gly Asp Ala Gly Val Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly
 260 265 270

ggc tgg ggt gcc cat ggt ggt ggt gcc ttc tct gga aag gac tac acc 864
 Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser Gly Lys Asp Tyr Thr
 275 280 285

aag gtg gac cgc tca gca gct tat gcc gcc cgc tgg gtg gcc aag tct 912
 Lys Val Asp Arg Ser Ala Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser
 290 295 300

ctg gtg aag gct ggg ctc tgc cgg aga gtc ctt gtt cag gtg tcc tat 960
 Leu Val Lys Ala Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr
 305 310 315 320

gcc att ggt gtg gca gaa cct ctg tcc att tcc att ttc acc tac gga 1008
 Ala Ile Gly Val Ala Glu Pro Leu Ser Ile Ser Ile Phe Thr Tyr Gly

325

330

335

act tcc aag aag acc gag cga gag cta cta gag gtt gtg aac aag aac 1056

Thr Ser Lys Lys Thr Glu Arg Glu Leu Leu Glu Val Val Asn Lys Asn

340

345

350

ttt gac ctc cgg ccg ggt gtt att gtc agg gac ttg gat ctg aag aag 1104

Phe Asp Leu Arg Pro Gly Val Ile Val Arg Asp Leu Asp Leu Lys Lys

355

360

365

ccc atc tac cag aag act gca tgc tat ggt cat ttc gga aga agc gag 1152

Pro Ile Tyr Gln Lys Thr Ala Cys Tyr Gly His Phe Gly Arg Ser Glu

370

375

380

ttt ccc tgg gag gtc ccc aag aag ctt gtg ttt 1185

Phe Pro Trp Glu Val Pro Lys Lys Leu Val Phe

385

390

395

<210> 11

<211> 395

<212> PRT

<213> Rattus norvegicus

<400> 11

Met Gly Pro Val Asp Gly Leu Cys Asp His Ser Leu Ser Glu Glu Gly
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Ala Phe Met Phe Thr Ser Glu Ser Val Gly Glu Gly His Pro Asp Lys
20 25 30

Ile Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala His Leu Lys Gln
35 40 45

Asp Pro Asn Ala Lys Val Ala Cys Glu Thr Val Cys Lys Thr Gly Met

50

55

60

Val Leu Leu Cys Gly Glu Ile Thr Ser Met Ala Met Ile Asp Tyr Gln

65

70

75

80

Arg Val Val Arg Asp Thr Ile Lys His Ile Gly Tyr Asp Asp Ser Ala

85

90

95

Lys Gly Phe Asp Phe Lys Thr Cys Asn Val Leu Val Ala Leu Glu Gln

100

105

110

Gln Ser Pro Asp Ile Ala Gln Cys Val His Leu Asp Arg Asn Glu Glu

115

120

125

Asp Val Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asp

130

135

140

Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Val Leu Ala His Lys Leu

145

150

155

160

Asn Thr Arg Met Ala Asp Leu Arg Arg Ser Gly Val Leu Pro Trp Leu

165

170

175

Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln Tyr Val Gln Asp Asn

180

185

190

Gly Ala Val Ile Pro Val Arg Val His Thr Ile Val Ile Ser Val Gln

195

200

205

His Asn Glu Asp Ile Thr Leu Glu Ala Met Arg Glu Ala Leu Lys Glu

210

215

220

Gln Val Ile Lys Ala Val Val Pro Ala Lys Tyr Leu Asp Glu Asp Thr

225

230

235

240

Ile Tyr His Leu Gln Pro Ser Gly Arg Phe Val Ile Gly Gly Pro Gln

245

250

255

Gly Asp Ala Gly Val Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly

260

265

270

Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser Gly Lys Asp Tyr Thr

275

280

285

Lys Val Asp Arg Ser Ala Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser

290

295

300

Leu Val Lys Ala Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr

305

310

315

320

Ala Ile Gly Val Ala Glu Pro Leu Ser Ile Ser Ile Phe Thr Tyr Gly

325

330

335

Thr Ser Lys Lys Thr Glu Arg Glu Leu Leu Glu Val Val Asn Lys Asn

340

345

350

Phe Asp Leu Arg Pro Gly Val Ile Val Arg Asp Leu Asp Leu Lys Lys

355

360

365

Pro Ile Tyr Gln Lys Thr Ala Cys Tyr Gly His Phe Gly Arg Ser Glu

370

375

380

Phe Pro Trp Glu Val Pro Lys Lys Leu Val Phe

385

390

395